

SEQUENCE LISTING

(i) GENERAL INFORMATION:

(i) APPLICANT: Fruskin, Michael J.
Finger, Douglas J.
Picarella, Dominic
Lewman, Walter

(ii) TITLE OF INVENTION: Mucosal Vascular Addressins and Uses
Thereof

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Hariton, Brody, Smith & Reynolds, P.C.
P. O. BOX: Two Milntia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
PHONE: 542-1470

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DCS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08,875,849
(B) FILING DATE: 11-PEP-1996
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08,523,004
(B) FILING DATE: 11-SEP-1995

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08,386,357
(B) FILING DATE: 10-FEB-1995

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: Brody, David E.
(B) REGISTRATION NUMBER: 21,592
(C) REFERENCE, DOCKET NUMBER: LKS94-04A2

(x) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 731-361-6240
(B) TELEFAX: 731-361-9540

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GAT TGC GCA CTC GCC CTC CTG CTC GGG GGG CTT CTG GGG CTC CTC 48
Met Asp Phe Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu Leu
1 ! 10 15

CTC GGC CAG TCC CTC CAG GTC AAG CCC CTG CAG GTG GAG CCC CCG GAG 96
Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu
21 25 30

CCG GTG GCG GTG GCG TTG GGC GCG TCG CGC CAG CTC ACC TGC CGC 144
Pro Val Val Ala Val Ala Leu Gln Ala Ser Arg Gln Leu Thr Cys Arg
35 40 45

CTG GGC TCG GCG GAC CGC GGG GCG TCG GTG CAG TGG CGG GGC CTG GAC 192
Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp
50 55 60

ACC AGC CTC GGC GCG GCG CAG TCG GAC AGC GGC CGC AGC GTC CTC ACC 240
Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr
65 70 75 80

GTG CGG AAC GCG TCG TCG CGG GCG GCG ACC CGC GTG TGC GTG GGC 288
Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly
85 90 95

TCC TGC GGC GGC CGC ACC TTC CAG CAC AAG GAG CAG CTC CTT GTG TAC 336
Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr
100 105 110

GCG TTC CGG GAC CAG CTG ACC GTG TCC CCA GCA ACC CTG GTG CCT GGT 384
Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly
115 120 125

GAC CGG GAG GIG GCG TGT ACG GCG CAC AAA GTC ACG CCC GTG GAC CCC 432
Asp Pro Gln Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro
130 135 140

AAC CGG CTC TCC TTC TCC CTG CTC GTC GCG GGC CAG GAA CTG SAG GGG 480
Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly
145 150 155 160

GGG CAA GCC CTG GGC CCG GAG GTG CAG GAG GAG GAG GAG CCC TAC 618
Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Pro Gln
166 170 174

GGG GAC GAG GAC GTG CTG TTC AGG GTG ACA GAG GGT TCG CTC TCG ATG 626
Gly Asp Gln Asp Val Leu Thr Arg Val Thr Gln Ala Thr Lys Arg Leu Ile
180 184 188

CCC CTG GGG ACC CCT GTC CCG CCC GCC CTC TAC TGC CAG GCC ATG ATG 634
Pro Leu Gly Thr Pro Val Pro Ala Leu Tyr Cys Gln Ala Thr Met
195 200 205

AGG CTG CCT GGC TTG CAG CTC AGC CAC CCC CAG GCC ATC CCC GTC CTG 642
Arg Leu Pro Gly Leu Leu Ser His Arg Gln Ala Ile Pro Val Leu
210 215 220

CAC AGC CCG ACC TCC CCG GAG CCT CCC GAC ACC ACC TCC CCG GAG CCT 650
His Ser Pro Thr Ser Pro Glu Pro Asp Thr Thr Ser Pro Glu Pro
225 230 235 240

CCC AAC ACC ACC TCC CCG GAG TCT CCC GAC ACC ACC TCC CCG GAG CCT 658
Pro Asn Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Pro Glu Ser
245 250 255

CCC GAC ACC ACC TCC CAG GAG CCT CCC GAC ACC ACC TCC CAG GAG CCT 666
Pro Asp Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro
265 270 275

CCC GAC ACC ACC TCC CAG GAG CCT CCC GAC ACC ACC TCC CAG GAG CCT 674
Pro Asp Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro
275 280 285

CCC GAC ACC ACC TCC CAG GAG CCT CCC GAC ACC ACC TCC CAG GAG CCT 682
Pro Asp Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro
295 300 305

CCC GAC ACC ACC TCC CAG GAG CCT CCC GAC ACC ACC TCC CAG GAG CCT 690
Pro Asp Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro
310 315 320

ACC CCC AGG AGC CCA GGC TCC ACC AGG ACT CGC CGC CCT GAG ATC TCC 698
Thr Pro Arg Ser Pro Glu Pro Ala Pro Gln Gln Gly Ser Thr His
325 330 335

CAG GCT GGG CCT ACG CAG GGA GAA GTG ATC CCA ACA GGC TCG TCC AAA 706
Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly Ser Ser Lys
340 345 350

CCT CGG GGT GAC CAG CTG CCC GCG GCT CTG TGG ACC AGC AGT GCG GTG 714
Pro Ala Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser Ser Ala Val
355 360 365

CTG GGA CTG CTG CTC CTG GCC TTG CCC ACG TAT CAC CTC TGG AAA CGC 722
Leu Gly Leu Leu Leu Ala Leu Pro Thr Tyr His Leu Trp Lys Arg
365 370 375

TGC CGG CAC CIG GCT GAG GAC GAC ACC SAC CCA CCA GCT TCT CTG AGG 730
Cys Arg His Leu Ala Glu Asp Asp Thr His Pro Pro Ala Ser Leu Arg
370 375 380

CTT CTG CCC CAG GTG TCG GCC TGG GCT GGG TTA ARG GGG ACC GGC CAG 1100
Leu Leu Pro Gln Val Ser Ala Trp Ala Gly Leu Arg Gly Thr Gly Gln
120 390 395 400

GTC GGG ATC AGC CCC TCC TGAGTGGCCA GCTTTCCCG CTGTGAAAC 1148
Val Gly Thr Ser Pro Ser
405X

AAAATAGCTT GGACCCCTTC AAGTTGAGAA CTGGTCAGGG CAAACCTTCTT TCCCATTTA 1187
CTCAAAGTCA TCCCTCTGCT CACAGAGATG GATGCATGTT CTGATTGCCP CTTTGAGAA 1236
GCTCATCAGA AACTAAAAAG AAGGCCACTG TTTGTCTCAC CTACCCATGA CCTGAAKCN 1426
CTCCCTGAGT GGTCCCCACC TTTCTGGACG GAACCACGTA CTTTTTACAT ACATTGATTC 1488
ATGTCTCAGG TCTCCCTAAA AATGCCCTAAG ACCAAGCTGT GGCCTGACCA CCCCTGCGCC 1544
CTGTCGTCAG GACCTCCCTGA GGCTTGGCA AATAAACCTC CTAANATGAT AAAAAAAA 1606
AAAAAAA AAVAAA 1624

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
A) LENGTH: 406 amino acids
B) TYPE: amino acid
C) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Phe Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu Leu
1 5 10 15

Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu
20 25 30

Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg
35 40 45

Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp
50 55 60

Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr
65 70 75 80

Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly
85 90 95

Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Ieu Val Tyr
100 105 110

Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly
115 120 125

Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro
130 135 140

Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gin Glu Leu Glu Gly
145 150 155 160

Ala Glu Ala Leu Gly Pro Glu Val Glu Glu Glu Glu Pro Glu
165 170 175

Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Ile Pro
180 185 190

Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gin Ala Thr Met
195 200 205

Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gin Ala Ile Pro Val Leu
210 215 220

His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro
225 230 235 240

Pro Asn Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Pro Glu Ser
245 250 255

Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro
260 265 270

Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro
275 280 285

Pro Asp Lys Thr Ser Pro Glu Pro Ala Pro Gln Gln Gly Ser Thr His
290 295 300

Thr Pro Arg Ser Pro Gly Ser Thr Arg Thr Arg Arg Pro Glu Ile Ser
305 310 315 320

Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly Ser Ser Lys
325 330 335

Pro Ala Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser Ser Ala Val
340 345 350

Leu Gly Leu Leu Leu Ala Leu Pro Thr Tyr His Leu Trp Lys Arg
355 360 365

Cys Arg His Leu Ala Glu Asp Asp Thr His Pro Pro Ala Ser Leu Arg
370 375 380

Leu Leu Pro Gln Val Ser Ala Trp Ala Gly Leu Arg Gly Thr Gly Gln
385 390 395 400

Val Gly Ile Ser Pro Ser
405

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TECHNOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GAT TIC GGA CTG GCG CTC CTG CTG GCG CCG CTT CTG GGG CTC CTC 45
Met Asp Ile Glu Leu Ala Ile Leu Leu Ala Gly Leu Leu Gly Leu Leu
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865

CTC GGC CAG TCG CTC CA; GTG AAG CCC CTG CAG GTG GAG CCC CCG GAG 96
Leu Gly Gln Se: Leu Glu Val Lys Pro Leu Gln Val Glu Pro Pro Glu
2 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865

CCG GTG GTG GC; GTG GC; TTG GGC GCG TCG CGC CAG CTC ACC TGC CGC 144
Pro Val Val Ala Val Al; Leu Glu Ala Ser Arg Gln Leu Thr Cys Arg
35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865

CTG GCC TGC GC; GAC CG; GGG GC; TCG GTG CAG TGG CGG GGC CTG GAC 192
Leu Ala Cys Ala Asp Arg Glu Ala Ser Val Gln Trp Arg Gly Leu Asp
55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865

ACC AGC CTG GGC GCG GTG CAG TCG GAC ACG CGC CGC AGC GTC CTC ACC 240
Thr Ser Leu Glu Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr
65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865

GTG CGC AAC GCG TCG CTG TCG CGC GCG GGG ACC CGC GTG TGC GTG GGC 288
Val Arg Asn Ala Ser Leu Se: Ala Ala Gly Thr Arg Val Cys Val Gly
35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865

TCC TGC GGG CGC CGC ACC TTC CAG CAC ACC GTG CAG CTC CTT GTG TAC 336
Ser Cys Gly Glu Arg Thr Phe Glu His Thr Val Gln Leu Leu Val Tyr
100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865

GCC TTC CCG CAG CAG CTG ACC GTC TCC CCA GCA GCC CTG GTG CCT GGT 384
Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly
115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865

CAC CCG GAG GTG GCC TGT ACG GCC CAC Ala GTC ACG CCC GTG GAC CGC 432
Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro
110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865

AAC GCG CTC TCC TTC CTG CTC GTC GGG GGC CAG GAA CTG GAG GGG 480
Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Glu Gln Glu Leu Glu Gly
145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865

5ATGCATGATCTGATTGCTCTTGGAGAA GCTCATCAGAACCTAAAAG AACGGAA TTT
TTT GCTTCACTTAAAGATGA CCTGAAACCCCTTCCTGACT GCTGCCACCTTTTGACG
AAACACGTA CTTTTACATACATTGATTCATGCTCAGG TCTCCCTAAA AATTCGAAAG
ACAGAGCTGCTGACCA CCCTGGGGCTCTGCTGCTGAG GATTCGAAAG GCTTGGAA
AATAAACCTC CTAATGAA AAAAAAAA AAA

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Phe Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu Leu
1 5 10 15
Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu
20 25 30
Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg
35 40 45
Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp
50 55 60
Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr
65 70 75 80
Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly
85 90 95
Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr
100 105 110
Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly
115 120 125
Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro
130 135 140
Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly
145 150 155 160
Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Pro Gln
165 170 175
Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro
180 185 190

Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Glu Ala Thr Met
195 200 205

Arg Leu Pro Gly Leu Glu Leu Ser His Arg Glu Ala Pro Ile Val Ile
210 215 220

His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Ser
225 230 235 240

Pro Asp Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Glu Glu Pro
245 250 255

Pro Asp Thr Thr Ser Pro Glu Pro Pro Asp Lys Thr Ser Pro Glu Pro
260 265 270

Ala Pro Gln Gln Gly Ser Thr His Thr Pro Arg Ser Pro Gly Ser Thr
275 280 285

Arg Thr Arg Arg Pro Glu Ile Ser Glu Ala Gly Pro Thr Glu Gly Glu
290 295 300

Val Ile Pro Thr Gly Ser Ser Lys Pro Ala Gly Asp Gln Leu Pro Ala
305 310 315 320

Ala Leu Trp Thr Ser Ser Ala Val Leu Gly Leu Leu Leu Leu Ala Leu
325 330 335

Pro Thr Tyr His Leu Trp Lys Arg Cys Arg His Leu Ala Glu Asp Asp
340 345 350

Thr His Pro Pro Ala Ser Leu Arg Leu Leu Pro Gln Val Ser Ala Trp
355 360 365

Ala Gly Leu Arg Gly Thr Gly Glu Val Gly Ile Ser Pro Ser
370 375 380

(2) INFORMATION FCP SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1721 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..1038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGC ATG GAT CGG GGC CTG GCG CTC CTG CTG GCG GGG CTT CTG GGG CTC
Met Asp Arg Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu
1 5 10 15

ATC GAG CCC GGC TGC GGC CAG TCC CTC CAG GTG AAG CCG CTC CAG GTC Leu Gln Pro Gly Cys Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val	36
20 35 40 45	30 35 40 45
GAG CCC CCT GAG CGG GTG GTC GGC CTC CTC CAG CTC CTC CAG CTC CTC CAG Gln Pro Pro Gln Pro Val Val Ala Val Ala Leu Gly Ala Ser Asp Thr Val	146
35 40	40 45
CTC ACC TGC CGC CTG GAC TCC CCG GAC CCC GGG GGC ACC GTG GAG TCG Leu Thr Cys Arg Leu Asp Cys Ala Asp Arg Gly Ala Thr Val Gln Thr	147
50	55
CGG CGC CTC GAC ACC AGG CTG CGC GCG GTG CAG TCG GAC GCG GGC CGC Arg Gly Leu Asp Thr Ser Leu Gly Ala Val Gln Ser Asp Ala Gly Arg	240
65 70	75
AGC GTC CTC ACC GTG CGC AAC GCC TCG CTG TCG CGG GCC GCG ACC CGT Ser Val Leu Thr Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg	288
80 85	90 95
GTC TGC GTC GGC TCC TGC GGG GGC CGC ACC TTC CAG CAC ACC GTG CGG Val Cys Val Gly Ser Cys Gly Arg Thr Phe Gln His Thr Val Arg	336
100 105	110
CTC CTT GTC TAC GC : TTC CCG GAG CAG CTG ACC ATC TCC CCG GCA GCC Leu Leu Val Tyr Alc Phe Pro Asp Gln Leu Thr Ile Ser Pro Ala Ala	384
110 120	125
CTG GCG CCT GGT GAC CGG GAG GTG GCG TGT ACG GCG CAC AAA GTC ACG Leu Val Pro Gly Asp Pro Gln Val Ala Cys Thr Alc His Lys Val Thr	432
130 140	140
CCT GTG GAC CGC AAT GCG CTC TCC TTC TAC CTG CT : CTG GGG GAC CAG Pro Val Asp Pro Asn Ala Leu Ser Phe Ser Leu Leu Gly Asp Gln	480
145 155	155
GAA CTG GAT GGG CGC CAG GCT CTG GGC CTC GAG GAG GAG GAG GAG GAG Glu Leu Gln Gly Ala Gln Ala Leu Gly Pro Gln Val Gln Glu Glu	528
160 165	170 175
GAG GAG CCT CAG GAG GAG GAC GTC CTC AG : GTG ACA GAG CGC Glu Gln Pro Gln Glu Glu Gln Asp Val Leu Phe Alc Val Thr Glu Arg	576
180 185	190
GGG DGG CTG CGC ACC CTG GCA ACC CCT GTC CTG CCT GCG CTC TAC TGC Trp Arg Leu Pro Thr Leu Ala Thr Pro Val Leu Pro Ala Leu Tyr Cys	624
195 200	205
CAG GGC ACG ATG AGG CTG CCT GGC TTG GAG CTC AGC CA : CGC CAG GCC Gln Ala Thr Met Arg Leu Pro Gly Leu Gln Leu Ser His Arg Gln Ala	672
210 215	220
ATC CGG GTG CTG CAC GGC CGC ACC TCC CGG GAG CCC CCT GAG ACG ACC Ile Pro Val Leu His Gly Pro Thr Ser Arg Glu Pro Pro Asp Thr Thr	720
225 230	235
TCC CGG GAA CGC CGG GCG ACC TCC CGG GAG ACC ACC CCC CAG CAG Ser Pro Glu Pro Arg Ala Ala Thr Ser Pro Glu Thr Thr Pro Gln Gln	768
240 245	250 255

GGT TCC ACA CAC AGC CCC AGG AGC CCG GGC TCT ACC ARG ALP TGC TGT 816
Gly Ser Thr His Ser Pro Arg Ser Pro Gly Ser Thr Arg Thr Cys Arg
260 265 270

CCT GAG ATC TCC CAG GCT GCG CCC AGG GAG GGA GAA GIG ATC TGA AIA 840
Pro Glu Ile Ser Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr
275 280 285

ATG TGA TCC AAA CCT ACG GCT GAC CAG CTG CCC GCG GCT CTC TCG ACG 864
Gly Ser Ser Lys Pro Thr Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr
290 295 300

AGC AGT GCG GTG CTG CGA CTG CTG CTC CTG CCT TTG CCC ATC TAC TAC 880
Ser Ser Ala Val Leu Gly Leu Leu Leu Ala Leu Pro Thr Tyr His
305 310 315

CTC TGG AAA CGT TGC CGG CAC CTG GCT GAG GAC GGC GCC CAC CCA CCA 1008
Leu Trp Lys Arg Cys Arg His Leu Ala Glu Asp Gly Ala His Pro Pro
320 325 330 335

GCT TCT CTC AGT AGC CAG CCC CTG TGAAGGGAAA ATAGGTTGGA 1058
Ala Ser Leu Ser Ser Gln Pro Phe Pro Leu
340 345

CCCCTTCAAG CTGAGAAGTG GTCTGGGCAAA ACCTGCCTCC CATTCTATTC AAAGTCATCG 1118
CTCTGGTCAC AGAGAGGAGAC GCACATTCTG ATTGCCTCCT TTGGAAAGGC TCATCAGAAA 1178

CTCAAAAGAA GGTGATGTT TGTCCCGCCT ACCCGTGACCC TGGAAGCCCC CGCCCCGCTC 1238
GAGTGACCCCG TGACCTTCTG GACGGAAACCA ACGTACTTCT TACATATATT GATTCATGTG 1298

TCATATCTCC CTAAAATCG TAAAACCGC TGTGCCCGA CCACCTTGGG CCCCTGCCAT 1358
CAGGACCTCC TGAGGCTTGT GCAATAAAC CGCTAAAG GATAAAACT GAAACTTGTG 1418
GCGGGCGCG GTGGCTAAAG CCTGTAATCC CAGGACTTTG GGAGGCCGAG GTGGGTGGAT 1478
CACGAGGTCA GGAGATGGAG ACCATGCTGG CTAAACCGTG AAACCCCGT TCTACTAAAA 1538
AAATACAAAAA ATTAGGGGG AGGGTGGCG GGGGCGCTGTA GTCCCGCTA CTGGGAGGC 1598
TGAGGCAGGA GAATGGCTG AACCGGGGAG GCGGAGCTG CAGTGAGCTG AGATCCGGCC 1658
ACTGCACTCC AGCCTGGGG ACAAGCGAG ACTCCGTCTC AAAAAAAA AAAAAAAA 1718
AAA 1721

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Asp Arg Cys Gly Leu Ala Leu Leu Ala Gly Leu Leu Ser Gly
1 5 10 15

Gly Pro Gly Cys Gly Gin Ser Leu Gln Val Lys Pro Leu Gln Val Gln
20 25 30

Pro Pro Gln Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu
35 40 45

Thr Cys Arg Leu Asp Cys Ala Asp Arg Gly Ala Thr Val Gln Trp Arg
50 55 60

Gly Leu Asp Thr Ser Leu Gly Ala Val Gin Ser Asp Ala Gly Arg Ser
65 70 75 80

Val Leu Thr Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val
85 90 95

Cys Val Gly Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Arg Leu
100 105 110

Leu Val Tyr Ala Phe Pro Asp Gln Leu Thr Ile Ser Pro Ala Ala Leu
115 120 125

Val Pro Gly Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro
130 135 140

Val Asp Pro Asn Ala Leu Ser Phe Ser Leu Leu Gly Asp Gln Glu
145 150 155 160

Leu Glu Gly Ala Gln Ala Leu Gly Pro Glu Val Glu Glu Glu Glu
165 170 175

Glu Pro Gln Glu Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp
180 185 190

Arg Leu Pro Thr Leu Ala Thr Pro Val Leu Pro Ala Leu Tyr Cys Gln
195 200 205

Ala Thr Met Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile
210 215 220

Pro Val Leu His Gly Pro Thr Ser Arg Glu Pro Pro Asp Thr Thr Ser
225 230 235 240

Pro Glu Pro Arg Ala Ala Thr Ser Pro Glu Thr Thr Pro Gln Gln Gly
245 250 255

Ser Thr His Ser Pro Arg Ser Pro Gly Ser Thr Arg Thr Cys Arg Pro
260 265 270

Glu Ile Ser Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly
275 280 285

Ser Ser Lys Pro Thr Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser
290 295 300

Arg Ala Val Leu Gly Leu Leu Leu Ala Leu Pro Thr Tyr His Leu
300 310 315 320 330 335 340 345

Trp Lys Arg Cys Arg His Leu Ala Glu Asp Gly Ala His Pro Pro Ala
320 330 335

Arg Leu Arg Arg Glu Asp Pro Leu Pro Leu
340 345

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTCTACTGCC AGGDAAG

18

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGCCTGGGAG ATCTTAAGG

19

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCCACGATGA AGCTGCTGG

20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GT GAA GCT TCC ACC ACG ATT TCG GAC TGG C CC

20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAAAGCTTCC ACC ACG ATT TCG GAC TGG C CC

21

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCGACTAGTG TCGG AGCTTG TGGAG

26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGACTAGTGG TTTAGAGAG TCTGTTC

27

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gly Leu Asp Thr Ser Leu
1 5

(1) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

A) NAME/KEY: Region
B) LOCATION: 2
D) OTHER INFORMATION: /product= "OTHER"

/label= variable

/note= "Xaa = Leu or Leu"

(ix) FEATURE:

A) NAME/KEY: Region
B) LOCATION: 3
D) OTHER INFORMATION: /product= "OTHER"

/label= variable

/note= "Xaa = Asp or Glu"

(ix) FEATURE:

A) NAME/KEY: Region
B) LOCATION: 4
D) OTHER INFORMATION: /product= "OTHER"

/label= variable

/note= "Xaa = Thr or Ser"

(ix) FEATURE:

A) NAME/KEY: Region
B) LOCATION: 5
D) OTHER INFORMATION: /product= "OTHER"

/label= variable

/note= "Xaa = Pro or Ser"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Xaa Xaa Xaa Xaa Leu
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gln Thr Asp Thr Leu
1 5

(xii) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Asp Thr Ser Leu
1 5